

Davis, Minh-Tam

From: Davis, Minh-Tam
Sent: Monday, January 09, 2006 4:08 PM
To: Chan, Christina
Subject: Rush search request for 10/048046

- 1) Please search in commercial database, issued patent files and PGPUB:
A nucleic acid encoding SEQ ID NO:2, with size limitation for the sequences in the database to equal or less than 50 nucleotides.
- 2) Interference search only for:
 - a) SEQ ID NO:1
 - b) oligonucleotide search for SEQ ID NO:1, with size limitation for the sequences in the database to equal or less than 50 nucleotides.
 - c) A nucleic acid encoding SEQ ID NO:2.
 - d) oligonucleotide search for a nucleic acid encoding SEQ ID NO:2, with size limitation for the sequences in the database to equal or less than 50 nucleotides.

Thank you.
MINH TAM DAVIS
ART UNIT 1642, ROOM 3A24, MB 3C18
272-0830

QY 18 ArgLeuLeuArgLeuGlyAla 24
 Db 25 AGATGGCTCAGATTGGCGCT 5

RESULT 2

Sequence 104100, Application US/09396196G
 Patent No. 6821724

GENERAL INFORMATION:

APPLICANT: Michael Mittmann

APPLICANT: David Mack

APPLICANT: Affymetrix, Inc.

TITLE OF INVENTION: Methods of Genetic Analysis

FILE REFERENCE: 3101.1

CURRENT APPLICATION NUMBER: US/09/396,196G

CURRENT FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: 60/100,678

PRIOR FILING DATE: 1998-09-17

NUMBER OF SEQ ID NOS: 127805

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 104100

LENGTH: 25

TYPE: DNA

ORGANISM: mus musculus

US-09-396-196G-104100

Alignment Scores:
 Pred. No.: 148 Length: 25
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.05% Indels: 0
 DB: 3 Gaps: 0

US-10-048-046-2 (1-664) x US-09-396-196G-104100 (1-25)

QY 18 ArgLeuLeuArgLeuGlyAla 24
 Db 24 AGATGGCTCAGATTGGCGCT 4

RESULT 3

Sequence 104101, Application US/09396196G
 Patent No. 6821724

GENERAL INFORMATION:

APPLICANT: Michael Mittmann

APPLICANT: David Mack

APPLICANT: Affymetrix, Inc.

TITLE OF INVENTION: Methods of Genetic Analysis

FILE REFERENCE: 3101.1

CURRENT APPLICATION NUMBER: US/09/396,196G

CURRENT FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: 60/100,678

PRIOR FILING DATE: 1998-09-17

NUMBER OF SEQ ID NOS: 127805

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 104101

LENGTH: 25

TYPE: DNA

ORGANISM: mus musculus

US-09-396-196G-104101

Alignment Scores:
 Pred. No.: 148 Length: 25
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.05% Indels: 0
 DB: 3 Gaps: 0

QY 18 ArgLeuLeuArgLeuGlyAla 24
 Db 23 AGATGGCTCAGATTGGCGCT 3

RESULT 4

Sequence 104102, Application US/09396196G
 Patent No. 6821724

GENERAL INFORMATION:

APPLICANT: Michael Mittmann

APPLICANT: David Mack

APPLICANT: David Lockhart

APPLICANT: Affymetrix, Inc.

TITLE OF INVENTION: Methods of Genetic Analysis

FILE REFERENCE: 3101.1

CURRENT APPLICATION NUMBER: US/09/396,196G

CURRENT FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: 60/100,678

PRIOR FILING DATE: 1998-09-17

NUMBER OF SEQ ID NOS: 127806

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 104102

LENGTH: 25

TYPE: DNA

ORGANISM: mus musculus

US-09-396-196G-104102

Alignment Scores:
 Pred. No.: 148 Length: 25
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.05% Indels: 0
 DB: 3 Gaps: 0

QY 18 ArgLeuLeuArgLeuGlyAla 24
 Db 22 AGATGGCTCAGATTGGCGCT 2

RESULT 5

Sequence 104103, Application US/09396196G
 Patent No. 6821724

GENERAL INFORMATION:

APPLICANT: Michael Mittmann

APPLICANT: David Mack

APPLICANT: David Lockhart

APPLICANT: Affymetrix, Inc.

TITLE OF INVENTION: Methods of Genetic Analysis

FILE REFERENCE: 3101.1

CURRENT APPLICATION NUMBER: US/09/396,196G

CURRENT FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: 60/100,678

PRIOR FILING DATE: 1998-09-17

NUMBER OF SEQ ID NOS: 127806

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 104103

LENGTH: 25

TYPE: DNA

ORGANISM: mus musculus

QY 18 ArgLeuLeuArgLeuGlyAla 24
 Db 21 AGATGGCTCAGATTGGCGCT 1

US-10-048-046-2 (1-664) x US-09-396-1969-104103 (1-25)

QY 18 ArgLeuLeuArgLeuGlyAla 24
 Db 21 AGATGGCTGAGTTGGCCGT 1

RESULT 6

US-08-078-683A-35/C

Sequence 35, Application US/08078683A

GENERAL INFORMATION:

APPLICANT: Saunders, Scott

APPLICANT: Bernfield, Merton

APPLICANT: Kato, Masato

TITLE OF INVENTION: Construction and Use of Synthetic

SEQUENCE 35, Application US/08078683A

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 28 State Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII (text)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/078,683A

FILING DATE: 17-JUN-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Vincent, Matthew P.

REGISTRATION NUMBER: 36,709

REFERENCE/DOCKET NUMBER: CME-062

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLogy: linear

MOLECULE TYPE: cDNA

US-08-078-683A-35

Alignment Scores:

Pred. No.: 177

Score: 7.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 1.05%

DB: 2

Gaps: 0

US-10-048-046-2 (1-664) x US-08-471-970A-35 (1-30)

QY 623 SerGluLeuProValAlaVal 629

Db 26 TCCGAGTTCGGGTTGCAGTC 6

NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD
 STREET: 28 State Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA

Z1P: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII (text)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 08/078,683

FILING DATE: 17-JUN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Kato, Catherine J.

REGISTRATION NUMBER: P-41,106

REFERENCE/DOCKET NUMBER: CME-062

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLogy: linear

MOLECULE TYPE: cDNA

US-08-471-970A-35

| | |
|------------------------|---------|
| Alignment Scores: | |
| Pred. No.: | 177 |
| Score: | 7.00 |
| Percent Similarity: | 100.00% |
| Best Local Similarity: | 100.00% |
| Query Match: | 1.05% |
| DB: | 3 |
| Gaps: | 0 |

RESULT 8
 US-09-723-677B-35/C
 Sequence 35, Application US/09723677B
 Patent No. 6699368
 GENERAL INFORMATION:

APPLICANT: Saunders, Scott

APPLICANT: Bernfield, Merton

APPLICANT: Kato, Masato

TITLE OF INVENTION: CONSTRUCTION AND USE OF SYNTHETIC CONSTRUCTS ENCODING SYNDECAN

CURRENT APPLICATION NUMBER: US/09/723,677B

CURRENT FILING DATE: 2000-11-28

PRIOR APPLICATION NUMBER: 08471,970

PRIOR FILING DATE: 1995-06-06

PRIOR APPLICATION NUMBER: 08/078,683

PRIOR FILING DATE: 1993-06-17

PRIOR APPLICATION NUMBER: 07/856,869

PRIOR FILING DATE: 1992-03-24

PRIOR APPLICATION NUMBER: 07/757,654

PRIOR FILING DATE: 1991-09-05

PRIOR APPLICATION NUMBER: 07/746,797

PRIOR FILING DATE: 1991-08-12

PRIOR APPLICATION NUMBER: 07/731,585

RESULT 7

US-08-471-970A-35/C

Sequence 35, Application US/08471970A

Patient No. 6531295

GENERAL INFORMATION:

APPLICANT: Saunders, Scott

APPLICANT: Bernfield, Merton

APPLICANT: Kato, Masato

TITLE OF INVENTION: Construction and Use of Synthetic

TITLE OF INVENTION: Constructs Encoding Syndecan

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PRIORITY FILING DATE: 1989-03-29
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 35
LENGTH: 30
TYPE: DNA
ORGANISM: MUS SP
US-09-723-677B-35

Alignment Scores:
Pred. No.: 177 Score: 7.00 Percent Similarity: 100.00%
Best Local Similarity: 100.00% Query Match: 1.05%
DB: 3 TBLX: 6

RESULT 9
US-08-196-538-16
Sequence 16, Application US/08196538
Patent No. 5639608
GENERAL INFORMATION:
APPLICANT: Stanley C. Richardson
TITLE OF INVENTION: USE OF SHORT OLIGONUCLEOTIDES AS PRIMERS
TITLE OF INVENTION: FOR DNA SEQUENCING
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADRESSEEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: Wordperfect (version 5.1)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US08/196,538
FILING DATE: February 14, 1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/985,468
FILING DATE: December 13, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 206/090
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 33
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-582-740-6

Alignment Scores:
Pred. No.: 205 Score: 7.00 Percent Similarity: 100.00%
Best Local Similarity: 100.00% Query Match: 1.05%
DB: 3 TBLX: 7

RESULT 10
US-08-582-740-6
Sequence 6, Application US/08582740
Patent No. 6037324
GENERAL INFORMATION:
APPLICANT: Schwander, Charles F.
TITLE OF INVENTION: Inhibitors of MacCAM-1-Mediated
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADRESSEEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/582,740
FILING DATE: 04-JAN-1996
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Brook, David B.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS95-12
TELEPHONE: (617) 861-5240
TELEFAX: (617) 861-5540

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-582-740-6

Alignment Scores:
Pred. No.: 205 Score: 7.00 Percent Similarity: 100.00%
Best Local Similarity: 100.00% Query Match: 1.05%
DB: 3 TBLX: 7

RESULT 11
US-08-109-879-6
Sequence 6, Application US/09109879
Patent No. 6374556
GENERAL INFORMATION:
APPLICANT: Schwander, Charles F.
TITLE OF INVENTION: INHIBITORS OF MACCAM-1-MEDIATED
NUMBER OF INVENTION: INTERACTIONS AND METHODS OF USE THEREFOR

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NUMBER OF SEQUENCES: 89
 CORRESPONDENCE ADDRESS: Brook, Smith & Reynolds, P.C.
 STREET: Two Millita Drive
 CITY: Lexington
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02421
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/582,740
 FILING DATE: 04-JAN-1996
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Brock, David E.
 REGISTRATION NUMBER: 22,592
 REFERENCE/DOCKET NUMBER: LKS95-12A2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 861-6240
 TELEFAX: (781) 861-9540
 INFORMATION FOR SEQ ID NO: 6:
 LENGTH: 39 base pairs
 SEQUENCE CHARACTERISTICS:
 LENGTH: 39 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 FEATURES:
 NAME/KEY: CDS
 LOCATION: 1..39
 US-08-582-740-63
 ATTENTION: BROOK, DAVID E.
 REGISTRATION NUMBER: 22,592
 REFERENCE/DOCKET NUMBER: LKS95-12A2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 861-6240
 TELEFAX: (781) 861-9540
 INFORMATION FOR SEQ ID NO: 6:
 LENGTH: 35 base pairs
 SEQUENCE CHARACTERISTICS:
 LENGTH: 35 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-109-879-6
 ALIGNMENT SCORES:
 Pred. No.: 205 Length: 35
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.05% Indels: 0
 DB: 3 Gaps: 0
 US-10-048-046-2 (1-664) x US-08-582-740-63 (1-35)
 Qy 207 GlySerGlyGlyGlyGlyTle 213
 Qy 207 GlySerGlyGlyGlyGlyTle 213
 Db 24 GAACTGGGGAGGGATT 4
 RESULT 13
 US-09-109-879-63/C
 Sequence 63, Application US/03109879
 Patent No. 6274356
 GENERAL INFORMATION:
 APPLICANT: Schwander, Charles P.
 APPLICANT: Shroff, Hitesh N.
 TITLE OF INVENTION: INHIBITORS OF MACCAM-1-MEDIATED
 TITLE OF INVENTION: INTERACTIONS AND METHODS OF USE THEREFOR
 NUMBER OF SEQUENCES: 89
 CORRESPONDENCE ADDRESS:
 ADDRESSEES: Hamilton, Brook, Smith & Reynolds, P.C.
 STREET: Two Millita Drive
 CITY: Lexington
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02421
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/109,879
 FILING DATE: 02-JUL-1998
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 APPLICATION NUMBER: PCT/US97/00291
 FILING DATE: 03-JAN-1997
 ATTORNEY/AGENT INFORMATION:
 APPLICATION NUMBER: US 08/582,740
 FILING DATE: 04-JAN-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Brock, David E.
 REGISTRATION NUMBER: 22,592
 REFERENCE/DOCKET NUMBER: LKS95-12A2

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781) 861-6240
 TELEX/FAX: (781) 861-9540
 INFORMATION FOR SEQ ID NO: 63:

SEQUENCE CHARACTERISTICS:
 LENGTH: 39 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear

FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..39

US-09-109-879-63
 Alignment Scores:
 Pred. No.: 227
 Score: 7.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 1.05%
 DB: 3

US-10-048-046-2 (1-664) x US-07-931-473B-77 (1-39)
 OY 461 ProsertherSevalserLeu 467
 Db 22 CCTTCGACATCCGTGAGCTG 2

US-10-048-046-2 (1-664) x US-09-109-879-63 (1-39)

RESULT 15
 Sequence 109 Application US/07931473B
 Patent No. 5270163
 GENERAL INFORMATION:
 APPLICANT: Larry Gold
 APPLICANT: Craig Turk
 TITLE OF INVENTION: Nucleic Acid Ligands
 NUMBER OF SEQUENCES: 335
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Beaton & Swanson, P.C.
 STREET: 4582 South Ulster Street Parkway, #403
 CITY: Denver
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80237

RESULT 14
 Sequence 77 Application US/07931473B
 Patent No. 5270163
 GENERAL INFORMATION:
 APPLICANT: Larry Gold
 APPLICANT: Craig Turk
 TITLE OF INVENTION: Nucleic Acid Ligands
 NUMBER OF SEQUENCES: 335
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Beaton & Swanson, P.C.
 STREET: 4582 South Ulster Street Parkway, #403
 CITY: Denver
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80237

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 5.25 inch, 360 KB storage
 COMPUTER: IBM compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/931,473B
 FILING DATE: 19920817
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:
 NAME: Barry J. Swanson
 REGISTRATION NUMBER: 33,215
 REFERENCE/DOCKET NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 850-9900
 TELEFAX: (303) 850-9401
 INFORMATION FOR SEQ ID NO: 109:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 40 nucleotides
 TYPE: NUCLEIC ACID
 STRANDEDNESS: single
 TOPOLOGY: linear

US-07-931-473B-109

Alignment Scores:
 Pred. No.: 232
 Score: 7.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 1.05%
 DB: 2

US-10-048-046-2 (1-664) x US-07-931-473B-109 (1-40)
 OY 461 ProsertherSevalserLeu 467
 Db 22 CCTTCGACATCCGTGAGCTG 2

US-10-048-046-2 (1-664) x US-07-931-473B-109 (1-40)

Best Local Similarity: 100.00%
 Query Match: 1.05%
 DB: 2
 Mismatches: 0
 Indels: 0
 Gaps: 0

OY 461 ProsertherSevalserLeu 467
 Db 22 CCTTCGACATCCGTGAGCTG 2

US-10-048-046-2 (1-664) x US-07-931-473B-77 (1-40)

OY 461 ProsertherSevalserLeu 467
 Db 22 CCTTCGACATCCGTGAGCTG 2

Alignment Scores:
 Pred. No.: 232
 Score: 7.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 1.05%
 DB: 2

Search completed: January 12, 2006, 10:59:56
 Job time : 317 Secs

Alignment Scores:
 Pred. No.: 232
 Score: 7.00
 Percent Similarity: 100.00%
 Length: 40
 Matches: 7
 Conservative: 0
 Mismatches: 0
 Indels: 0
 Gaps: 0

Handwritten Note: Not for filing

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Db          1 ACCGTATGATCTGTCAGACCTT 24
RESULT 2
US-11-016-317-24277
; Sequence 24277, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIORITY FILING DATE: 2004-01-13
; PRIORITY APPLICATION NUMBER: US 60/536,639
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
; SEQ ID NO 24277
; LENGTH: 25

; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-24277

Alignment Scores:
Pred. No.: 72 Length: 25
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.20% Indels: 0
DB: 10 Gaps: 0

US-10-048-046-2 (1-664) x US-11-036-317-24277 (1-25)

QY 48 LeuSerPheProSerAsnLeu 55
      ||||| CTCCTTCCCCAGGATAACTG 24

Db 1 CTCCTTCCCCAGGATAACTG 24

RESULT 3
US-11-036-317-24394
; Sequence 24394, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/316,317
; CURRENT FILING DATE: 2005-01-13
; PRIORITY APPLICATION NUMBER: US 60/536,639
; PRIORITY FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 24394
; LENGTH: 25

; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-24394

Alignment Scores:
Pred. No.: 72 Length: 25
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.20% Indels: 0
DB: 10 Gaps: 0

US-10-048-046-2 (1-664) x US-11-036-317-60227 (1-25)

QY 49 SerPheProSerAsnLeuVal 56
      ||||| TCTTCCCCAGGATAACTGTC 24
Db 1 TCTTCCCCAGGATAACTGTC 24

RESULT 5
US-11-036-317-61246
; Sequence 61246, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIORITY FILING DATE: 2004-01-13
; PRIORITY APPLICATION NUMBER: US 60/536,639
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
; SEQ ID NO 61246
; LENGTH: 25

; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-61246

Alignment Scores:
Pred. No.: 72 Length: 25
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.20% Indels: 0
DB: 10 Gaps: 0

US-10-048-046-2 (1-664) x US-11-036-317-61246 (1-25)

QY 47 AspLeuSerPheProSerAsnLeu 54
      ||||| GACCTCTCTTCCCCAGGATAAA 25
Db 2 GACCTCTCTTCCCCAGGATAAA 25

RESULT 6
US-11-036-317-67592
; Sequence 67592, Application US/11036317
; Publication No. US20050214823A1

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/ GENERAL INFORMATION:
/   APPLICANT: Williams, Alan
/   APPLICANT: Blume, John
/   TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
/   FILE REFERENCE: 3654.1
/   CURRENT APPLICATION NUMBER: US/11/036,317
/   CURRENT FILING DATE: 2005-01-13
/   PRIOR APPLICATION NUMBER: US 60/536,639
/   CURRENT APPLICATION NUMBER: US/11/036,317
/   CURRENT FILING DATE: 2005-01-13
/   PRIOR FILING DATE: 2004-01-13
/   NUMBER OF SEQ ID NOS: 991174
/   SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/   SEQ ID NO: 67592
/   LENGTH: 25
/   TYPE: DNA
/   ORGANISM: Mus musculus
/   US-11-036-317-67592

Alignment Scores:
Pred. No.: 72 Length: 25
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.204 Indels: 0
DB: Gaps: 0

RESULT 7
US-11-036-317-108822
Sequence 108822, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 108822
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-108822

Alignment Scores:
Pred. No.: 72 Length: 25
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.204 Indels: 0
DB: Gaps: 0

RESULT 8
US-11-036-317-131760
Sequence 131760, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 131760
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-131760

Alignment Scores:
Pred. No.: 72 Length: 25
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.204 Indels: 0
DB: Gaps: 0

RESULT 9
US-11-036-317-144618
Sequence 144618, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 144618
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-144618

Alignment Scores:
Pred. No.: 72 Length: 25
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.204 Indels: 0
DB: Gaps: 0

RESULT 10
US-11-036-317-153103
Sequence 153103, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 153103
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-153103

Alignment Scores:
Pred. No.: 72 Length: 25
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.204 Indels: 0
DB: Gaps: 0

RESULT 11
US-11-036-317-17144618
Sequence 17144618, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 17144618
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-17144618

Alignment Scores:
Pred. No.: 72 Length: 25
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.204 Indels: 0
DB: Gaps: 0

```

```

CURRENT FILING DATE: 2005-01-13
PRIORITY APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
SEQ ID NO: 153103
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-153103

Alignment Scores:
Pred. No.: 72 Length: 25
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.20% Indels: 0
DB: Gaps: 0

US-10-048-046-2 (1-664) x US-11-036-317-153103 (1-25)
QY 405 BergluasplausGlueuser 412
Db 2 TCAGGAGCTGCTGAGCTCT 25

RESULT 11
US-11-036-317-166836
Sequence 166836, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
PRIORITY FILING DATE: 2004-01-13
PRIORITY APPLICATION NUMBER: US 60/536,639
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
SEQ ID NO: 166836
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-166836

Alignment Scores:
Pred. No.: 72 Length: 25
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.20% Indels: 0
DB: Gaps: 0

US-11-036-317-198348
Sequence 198348, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
PRIORITY FILING DATE: 2004-01-13
PRIORITY APPLICATION NUMBER: US 60/536,639
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
SEQ ID NO: 198348
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-198348

Alignment Scores:
Pred. No.: 72 Length: 25
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.20% Indels: 0
DB: Gaps: 0

US-10-048-046-2 (1-664) x US-11-036-317-198348 (1-25)
QY 42 ArgatArgatArglyCysBlauser 49
Db 2 AGGAGGGAGGCTGACCTCT 25

RESULT 13
US-11-036-317-233307
Sequence 233307, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
PRIORITY FILING DATE: 2005-01-13
PRIORITY APPLICATION NUMBER: US 60/536,639
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
SEQ ID NO: 233307
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-233307

Alignment Scores:
Pred. No.: 72 Length: 25
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.20% Indels: 0
DB: Gaps: 0

US-10-048-046-2 (1-664) x US-11-036-317-233307 (1-25)
QY 59 IleLeuIleValTyrLeuAlaThr 56
Db 2 ATCTGAGAGATTCTGGCAAC 25

RESULT 14
US-11-036-317-259770
Sequence 259770, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
PRIORITY FILING DATE: 2005-01-13
PRIORITY APPLICATION NUMBER: US 60/536,639
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
SEQ ID NO: 259770

```

```

    LENGTH: 25
    TYPE: DNA
    ORGANISM: Mus musculus
US-11-036-317-59770

```

```

Alignment scores:
Pred. No.:          72          Length: 25
Score:             8.00          Matches: 8
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:        1.20%  Indels: 0
DB:                10          Gaps: 0

```

US-10-048-046-2 (1-664) x US-11-036-317-259770 (1-25)

Qy 41 GYATGARGARGLYCysArgIleu 48
 Db 2 GAGAGGGGAGAGGCTGTGACCTC 25

RESULT 15

US-11-036-317-289125

Sequence 289125, Application US/11036317

Publication No. US20050214823A1

GENERAL INFORMATION:

APPLICANT: Williams, Alan

APPLICANT: Blume, John

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REFERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT FILING DATE: 2005-01-13

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR FILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 289125

LENGTH: 25

TYPE: DNA

ORGANISM: Mus musculus

US-11-036-317-289125

Alignment scores:

| Pred. No.: | 72 | Length: | 25 |
|------------------------|---------|---------------|----|
| Score: | 8.00 | Matches: | 8 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 1.20% | Indels: | 0 |
| DB: | 10 | Gaps: | 0 |

US-10-048-046-2 (1-664) x US-11-036-317-289125 (1-25)

Qy 558 AspIleLeuLysAsnTyrLeuAla 565
 Db 1 GACATTCGTGAGAAATTACCGCA 24

Search completed: January 12, 2006, 13:54:49
 Job time : 1361. sec(s)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model.

Run on: January 12, 2006, 10:56:48 / Search time 294 Seconds
(Without alignments)
1827.916 Million cell updates/sec

Title: US-10-048-046-2

Perfect score: 664

Sequence: 1 MERPEECKQSPPPQWGRLL.....VKAHHAMKPNHICBQTRPKN 664

Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgap 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6038814 seqs, 404674181 residues

Total number of hits satisfying chosen parameters: 11530093
Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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-DBPublished Applications NA New -QPRM=faster -SUPRICK oligo250_rnpn
-MINMATCH=0.1 -LOCCL=0 -LOCPXT=0 -UNITS=blts -SPARTL=-ENDL-1 -MATTX=0.1G
-ALIGN=15 -MODE=LOCAL -OUTPMT=PTO -NORM=ext -HEARSIZE=5500 -MINLEN=0 -MAXLEN=50
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-NO_MMAP -LAKESEQUERY -NEQ_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=7
-FGBEXT=7 -YGBOP=60 -YGBEXT=7 -DRGB6 -DRBEXT=7

Database 1 Published Applications NA New:

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10: /cgn2_6/podata/1/pubpna/us07_NEW_PUB_seq:*
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RESULT 1 US-10-310-914A-42895

Sequence 42895, Application US/10310914A

Publication No. US20060000322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

ATTORNEY: Shiler, Krutzat

TITLE OF INVENTION: Biologically detectable group of novel regulatory genes and

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION NUMBER: US10/310,914A

CURRENT FILING DATE: 2005-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn Version 3.3

SEQ ID NO: 42895

LENGTH: 21

TYPE: RNA

ORGANISM: Human

US-10-310-914A-42895

ALIGNMENTS

c 9 7 1.1 22 6 US-10-310-914A-1205143 Sequence 1205143,
c 10 7 1.1 23 6 US-10-310-914A-2890 Sequence 42890, A
c 11 7 1.1 23 6 US-10-310-914A-74831 Sequence 374831,
c 12 7 1.1 23 6 US-10-310-914A-48394 Sequence 48394,
c 13 7 1.1 23 6 US-10-310-914A-42344 Sequence 542344,
c 14 7 1.1 23 6 US-10-310-914A-815510 Sequence 815510,
c 15 7 1.1 23 6 US-10-310-914A-1320692 Sequence 1320692,
c 16 7 1.1 23 6 US-10-310-914A-1363452 Sequence 1363452,
c 17 7 1.1 24 6 US-10-310-914A-838918 Sequence 838918,
c 18 7 1.1 24 6 US-10-310-914A-1060225 Sequence 1060225,
c 19 7 1.1 24 6 US-10-310-914A-1228181 Sequence 1228181,
c 20 7 1.1 24 6 US-10-310-914A-1267239 Sequence 1267239,
c 21 7 1.1 24 6 US-10-310-914A-1363461 Sequence 1363461,
c 22 7 1.1 25 6 US-10-310-914A-97707 Sequence 97707, A
c 23 7 1.1 25 6 US-10-310-914A-222932 Sequence 222932,
c 24 7 1.1 25 6 US-10-310-914A-557609 Sequence 557609,
c 25 7 1.1 25 6 US-11-310-914A-1363459 Sequence 1363459,
c 26 7 1.1 25 7 US-11-121-849-239450 Sequence 239450,
c 27 7 1.1 25 7 US-11-121-849-321027 Sequence 321027,
c 28 7 1.1 25 7 US-11-121-849-321028 Sequence 321028,
c 29 7 1.1 25 7 US-11-121-849-415666 Sequence 415666,
c 30 7 1.1 25 7 US-11-121-849-415792 Sequence 412694,
c 31 7 1.1 25 7 US-11-121-849-421694 Sequence 421694,
c 32 7 1.1 25 7 US-11-121-849-428097 Sequence 428097,
c 33 7 1.1 25 7 US-11-121-849-428098 Sequence 428098,
c 34 7 1.1 25 7 US-11-121-849-568626 Sequence 568626,
c 35 7 1.1 26 6 US-10-310-914A-1004305 Sequence 1004305,
c 36 7 1.1 27 6 US-10-310-914A-815792 Sequence 815792,
c 37 7 1.1 27 6 US-10-310-914A-1004294 Sequence 1004294,
c 38 7 1.1 32 6 US-10-939-294A-16935 Sequence 16935, A
c 39 7 1.1 32 6 US-10-939-294A-17432 Sequence 17432,
c 40 7 1.1 32 6 US-10-939-294A-17619 Sequence 17619, A
c 41 7 1.1 32 6 US-10-939-294A-19324 Sequence 19324, A
c 42 6 0.9 18 6 US-10-310-914A-78818 Sequence 78818, A
c 43 6 0.9 18 6 US-10-310-914A-891188 Sequence 891188, A
c 44 6 0.9 18 6 US-10-310-914A-144700 Sequence 144700,
c 45 6 0.9 18 6 US-10-310-914A-176873 Sequence 176873,

SUMMARIES

Result No. Score Match Length DB ID Description

| Result No. | Score | Match | Length | DB ID | Description |
|------------|-------|-------|--------|------------------------|---------------------|
| 1 | 7 | 21 | 6 | US-10-310-914A-42895 | Sequence 42895, A |
| 2 | 7 | 1.1 | 21 | US-10-310-914A-42895 | Sequence 42895, A |
| 3 | 7 | 1.1 | 21 | US-10-310-914A-814306 | Sequence 814306, A |
| 4 | 7 | 1.1 | 21 | US-10-310-914A-1320691 | Sequence 1320691, A |
| 5 | 7 | 1.1 | 22 | US-10-310-914A-56004 | Sequence 56004, A |
| 6 | 7 | 1.1 | 22 | US-10-310-914A-374833 | Sequence 374833, A |
| 7 | 7 | 1.1 | 22 | US-10-310-914A-626661 | Sequence 626661, A |
| 8 | 7 | 1.1 | 22 | US-10-310-914A-1064918 | Sequence 1064918, A |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

159 of 114102

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Alignment scores:

| Pred. No.: | Score: | Length: | Matches: | Conservative: | Mismatches: | Gaps: |
|------------|---------|---------|----------|---------------|-------------|-------|
| 1 | 100.00% | 100.00% | 100.00% | 0 | 0 | 0 |
| 2 | 1.05% | 6 | 7 | 1 | 0 | 0 |

US-10-048-046-2 (1-664) x US-10-310-914A-42895 (1-21)

OY 150 GLYALAGLYLAGLYARGGLY 156

Db 1 GGGGGGGGGGGGGGGGU 21

RESULT 2

US-10-310-914A-638790/C

Sequence 638790, Application US/10310914A

Publication No. US20060003322A1 ✓

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Shlier, Kuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

TITLE OF INVENTION: uses thereof

FILR REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SEQ ID NO 638790

LENGTH: 21

TYPE: RNA

ORGANISM: Human

US-10-310-914A-638790

Alignment Scores:

Pred. No.: 380

Length: 21

Score: 7.00

Matches: 7

Percent Similarity: 100.00%

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

DB: 6

US-10-048-046-2 (1-664) x US-10-310-914A-638790 (1-21)

Qy 273 LeuValAlaGlnProArgArg 279 ✓

Db 21 CTTAGTGCCCCGCCCCGAGA 1

RESULT 3

US-10-310-914A-814306

Sequence 814306, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Shlier, Kuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

TITLE OF INVENTION: uses thereof

FILR REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SEQ ID NO 814306

LENGTH: 21

TYPE: RNA

ORGANISM: Human

US-10-310-914A-814306

Alignment Scores:

Pred. No.: 380

Length: 21

Score: 7.00

Matches: 7

Percent Similarity: 100.00%

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

DB: 6

US-10-048-046-2 (1-664) x US-10-310-914A-814306 (1-21)

Qy 150 GlyAlaGlyAlaGluArgArg 156 ✓

Db 1 GGCGCGCGCGCGCGAGGC 21

RESULT 4

US-10-310-914A-1320691/C

Sequence 1320691, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Shlier, Kuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

TITLE OF INVENTION: uses thereof

FILR REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SEQ ID NO 56004

LENGTH: 22

TYPE: RNA

ORGANISM: Human

US-10-310-914A-56004

Alignment Scores:

Pred. No.: 397

Length: 22

Score: 7.00

Matches: 7

Percent Similarity: 100.00%

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

DB: 6

US-10-048-046-2 (1-664) x US-10-310-914A-56004 (1-22)

Qy 495 ArgArgAlaGluArgGluGln 501 ✓

Db 21 AGGAGGGCTGAAGGGAGCA 1

RESULT 5

US-10-310-914A-56004/C

Sequence 56004, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Shlier, Kuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

TITLE OF INVENTION: uses thereof

FILR REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SEQ ID NO 56004

LENGTH: 22

TYPE: RNA

ORGANISM: Human

US-10-310-914A-56004

Alignment Scores:

Pred. No.: 397

Length: 22

Score: 7.00

Matches: 7

Percent Similarity: 100.00%

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

DB: 6

US-10-048-046-2 (1-664) x US-10-310-914A-56004 (1-22)

Qy 495 ArgArgAlaGluArgGluGln 501 ✓

Db 21 AGGAGGGCTGAAGGGAGCA 1

RESULT 6

US-10-310-914A-374833

Sequence 374833, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Shlier, Kuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

TITLE OF INVENTION: uses thereof

FILR REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SEQ ID NO 56004

LENGTH: 22

TYPE: RNA

ORGANISM: Human

US-10-310-914A-374833

Alignment Scores:

Pred. No.: 397

Length: 22

Score: 7.00

Matches: 7

Percent Similarity: 100.00%

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

DB: 6

US-10-048-046-2 (1-664) x US-10-310-914A-374833 (1-22)

Qy 150 GlyAlaGlyAlaGluArgArg 156 ✓

Db 1 GGCGCGCGCGCGCGAGGC 21

TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087_0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO: 374833
LENGTH: 22
TYPE: RNA
ORGANISM: Human
US-10-310-914A-374833

Alignment Scores:
Pred. No.: 397 Length: 22
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.05% Indels: 0
DB: Gaps: 0

US-10-048-046-2 (1-664) x US-10-310-914A-374833 (1-22)

Qy 150 GlyAlaGlyAlaGlyArgAlY 156
Db 2 GGGGGGGGGGGGGGGGGGG 22

RESULT 7
US-10-310-914A-626661
Sequence 626661, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087_0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO: 626661
LENGTH: 22
TYPE: RNA
ORGANISM: Human
US-10-310-914A-626661

Alignment Scores:
Pred. No.: 397 Length: 22
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.05% Indels: 0
DB: Gaps: 0

US-10-048-046-2 (1-664) x US-10-310-914A-626661 (1-22)

Qy 150 GlyAlaGlyAlaGlyArgAlY 156
Db 2 GGGGGGGGGGGGGGGGG 22

RESULT 8
US-10-310-914A-1064918/C
Sequence 1064918, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087_0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO: 42890
LENGTH: 23
TYPE: RNA
ORGANISM: Human

Alignment Scores:
Pred. No.: 397 Length: 22
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.05% Indels: 0
DB: Gaps: 0

US-10-310-914A-1064918
US-10-310-914A-1205143/C
Sequence 1205143, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087_0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO: 1205143
LENGTH: 22
TYPE: RNA
ORGANISM: Human
US-10-310-914A-1205143

Alignment Scores:
Pred. No.: 397 Length: 22
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.05% Indels: 0
DB: Gaps: 0

US-10-048-046-2 (1-664) x US-10-310-914A-1205143 (1-22)

Qy 156 GlyAlaAspProArgValPro 162
Db 21 GAGCCGACCTAGGTCCCC 1

RESULT 10
US-10-310-914A-42890
Sequence 42890, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087_0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO: 42890
LENGTH: 23
TYPE: RNA
ORGANISM: Human

US-10-310-914A-42890

Alignment Scores: 414
 Pred. No.: 7.00
 Score: 100.00%
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 1.05%
 DB: 6

US-10-048-046-2 (1-664) x US-10-310-914A-42890 (1-23)

Qy 150 GlyAlaGlyAlaGlyArgly 156
 Db 3 GGGGGGGGGGGGGGGGU 23

RESULT 11

Sequence 374831, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Shlier, Kvuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SEQ ID NO 374831

LENGTH: 23

TYPE: RNA

ORGANISM: Human

US-10-310-914A-374831

Alignment Scores:

Pred. No.: 414
 Score: 7.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 1.05%DB: 6
 Gaps: 0Length: 23
 Matches: 7
 Conservative: 0
 Mismatches: 0
 Indels: 0
 Gaps: 0

US-10-310-914A-374831 (1-23)

Qy 150 GlyAlaGlyAlaGlyArgly 156
 Db 1 GGGGGGGGGGGGGGU 21

RESULT 12

Sequence 482394, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Shlier, Kvuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SEQ ID NO 482394

LENGTH: 23

TYPE: RNA

ORGANISM: Human

US-10-310-914A-482394

Alignment Scores:

Pred. No.: 414
 Score: 7.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 1.05%

DB: 6

Length: 23
 Matches: 7
 Conservative: 0
 Mismatches: 0
 Indels: 0
 Gaps: 0

US-10-048-046-2 (1-664) x US-10-310-914A-42890 (1-23)

Qy 150 GlyAlaGlyAlaGlyArgly 156
 Db 3 GGGGGGGGGGGGGGU 23

RESULT 13

Sequence 542344, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Shlier, Kvuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SEQ ID NO 542344

LENGTH: 23

TYPE: RNA

ORGANISM: Human

US-10-310-914A-542344

Alignment Scores:

Pred. No.: 414
 Score: 7.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 1.05%DB: 6
 Gaps: 0Length: 23
 Matches: 7
 Conservative: 0
 Mismatches: 0
 Indels: 0
 Gaps: 0

US-10-048-046-2 (1-664) x US-10-310-914A-542344 (1-23)

Qy 184 LeuDheProThrAlaSerIle 190
 Db 23 CTGTCCCCACAGCCGCC 3

RESULT 14

Sequence 815510, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Shlier, Kvuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SEQ ID NO 815510

LENGTH: 23

TYPE: RNA

ORGANISM: Human

US-10-310-914A-815510

Alignment Scores:

Pred. No.: 414
 Score: 7.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 1.05%DB: 6
 Gaps: 0Length: 23
 Matches: 7
 Conservative: 0
 Mismatches: 0
 Indels: 0
 Gaps: 0

US-10-310-914A-815510 (1-23)

Qy 18 ArgLeuIuArgLeuGlyIala 24
 Db 3 AGGcUcUAcGccUuGggCU 23

US-10-048-046-2 (1-664) x US-10-310-914A-815510 (1-23)

Qy 150 GYAlaGlyAlaGlyArgGly 156
 Db |||||GGCAGGAGCTGGCCGGT 1

RESULT 15

US-10-310-914A-1320692/
 Sequence 1320692, Application US/10310914A
 Publication No. US2006003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

TITLE OF INVENTION: uses thereof
 FILE REFERENCE: 06087_0200.CPUS01CURRENT APPLICATION NUMBER: US/10/310,914A
 CURRENT FILING DATE: 2002-12-06NUMBER OF SEQ ID NOS: 1388402
 SEQ ID NO 1320692

SOFTWARE: Patentin version 3.3

TYPE: RNA

LENGTH: 23

ORGANISM: Human

US-10-310-914A-1320692

Alignment Score:
 Pred. No.: 414 Length: 23
 Score: -7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 6.05% Indels: 0
 DB: 6 Gaps: 0

US-10-048-046-2 (1-664) x US-10-310-914A-1320692 (1-23)

Qy 20 IleuArgLeuGlyAlaGluGlu 26
 Db |||||GGCAGGAGCTGGCCGGT 3

Search completed: January 12, 2006, 13:59:49
 Job time : 295 secs

GenCore version 5.1.6
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Om protein - nucleic search, using frame_plus_p2n model.

Run on: January 12, 2006, 10:25:28 / Search time 8800 Seconds

(without alignments)
 4088.375 Million cell updates/sec

Title: US-10-048-046-2
 Perfect score: 664
 Sequence: 1 MERPEECKQSPPPQPMRLL.....VKAHANKFNHICEQIRPKN 664

Scoring criteria

Xgapext 60.0 Xgapext 60.0
 Ygap 60.0 Ygapext 60.0
 Gapop 6.0 Rgapext 7.0
 Delop 6.0 Delet 7.0

Searched: 79147668 seqs, 27645789525 residues

Total number of hits satisfying chosen parameters: 87479736

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: listing first 45 summaries

Command line parameters:

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 -O/ cgn2_1/USP010008046/runat_10012006-122940_24149/app_query.fasta_1.839

-D=Pending Patients NA_Main -QPMTEFASTP -SUPPIXOLIG S250.RNP -MINMATCH=0.1

-L=LoopN -T=LoopBit -S=Start1 -End1 -MatrixOligo

-Trans=Human40_cdi -List=45 -DocAllIGN -THR_Min=1 -THR_Score=Quality -THR_Min=1

-AlignN=15 -ModB=Local -OutFormat=pto -NormExt -Heuristic=500 -MinLen=0 -MaxLen=50

-User=U91049046 seqn 1..1 7335 Arunat_10012006_12290_24149_NCPU6 -ICP=3

-No Map -LarkeQuery -NGC_Scores=0 -Wait -DeBlock=100 -LongLog

-Dev Timeout=120 -Warn Timeout=30 -Threads=1 -XgapPop=60 -XgapExt=60 -DelOp=6 -Delet=7

-RGAExt=7 -YgapPop=60 -YgapExt=60 -DelOp=6 -Delet=7

Database : Pending Patients NA_Main *

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 2: /cgns_2_6/podata/1/pna/PCUB_COMB.seq: *
 3: /cgns_2_6/podata/1/pna/PCURSC_COMB.seq: *
 4: /cgns_2_6/podata/1/pna/US06_COMB.seq: *
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 6: /cgns_2_6/podata/1/pna/US076_COMB.seq: *
 7: /cgns_2_6/podata/1/pna/US078_COMB.seq: *
 8: /cgns_2_6/podata/1/pna/US078_COMB.seq: *
 9: /cgns_2_6/podata/1/pna/US079_COMB.seq: *
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 23: /cgns_2_6/podata/1/pna/U9104_COMB.seq: *
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 26: /cgns_2_6/podata/1/pna/U9106_COMB.seq: *
 27: /cgns_2_6/podata/1/pna/U9108_COMB.seq: *
 28: /cgns_2_6/podata/1/pna/U9109_COMB.seq: *

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------------------------|-------------------|
| C 1 | 8 | 1.2 | 25 | 37 US-09-933-5708-36915 | Sequence 38015, A |
| C 2 | 8 | 1.2 | 25 | 37 US-09-934-4278-23035 | Sequence 218351, |
| C 3 | 8 | 1.2 | 25 | 37 US-09-934-4278-23035 | Sequence 218351, |
| C 4 | 8 | 1.2 | 25 | 37 US-09-934-4278-23035 | Sequence 218351, |
| C 5 | 8 | 1.2 | 25 | 37 US-09-934-4278-23035 | Sequence 218351, |
| C 6 | 8 | 1.2 | 25 | 38 US-09-936-6048-29770 | Sequence 29770, A |
| C 7 | 8 | 1.2 | 25 | 38 US-09-936-6048-29770 | Sequence 29770, A |
| C 8 | 8 | 1.2 | 25 | 38 US-09-936-6048-29770 | Sequence 29770, A |

RESULT 2
US-09-954-427A-238351
; Sequence 238351, Application US/09954427A
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat Genome
; FILE REFERENCE: 3112.1
; CURRENT APPLICATION NUMBER: US/09/954,427A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/233,166
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 238351
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus Norvegicus
; US-09-954-427A-238351
Sequence 62496, A
Sequence 62496, A
Alignment Scores:
Pred. No.: 716 Length: 25
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.20+ Indels: 0
DB: 37 Gaps: 0
US-09-954-427A-238353
Sequence 238353, Application US/09954427A
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat Genome
; FILE REFERENCE: 3112.1
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/233,166
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: Microarray Probe Sequence Listing Generator-V 1.1
; SEQ ID NO: 238353
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus Norvegicus
; US-09-954-427A-238353
Alignment Scores:
Pred. No.: 716 Length: 25
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.20+ Indels: 0
DB: 37 Gaps: 0
US-10-048-046-2 (1-664) x US-09-954-427A-238353 (1-25)
; Sequence 238358, Application US/09954427A
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat Genome

RESULT 1
US-09-953-570A-36815C
; Sequence 36815, Application US/09953570A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods or Genetic Analysis of Yeast
; FILE REFERENCE: 3110.1
; CURRENT APPLICATION NUMBER: US/09/953,570A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/233,638
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 138410
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 36815
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; US-09-953-570A-36815
Alignment Scores:
Pred. No.: 716 Length: 25
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.20+ Indels: 0
DB: 37 Gaps: 0
US-10-048-046-2 (1-664) x US-09-953-570A-36815 (1-25)
; Sequence 238358, Application US/09954427A
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat Genome

```

FILE REFERENCE: 3112.1
CURRENT APPLICATION NUMBER: US/09/954,427A
CURRENT FILING DATE: 2001-09-17
PRIORITY NUMBER: 60/233,166
PRIORITY FILING DATE: 2000-09-18
NUMBER OF SEQ ID NOS: 420907
SEQ ID NO 238358
LENGTH: 25
TYPE: DNA
ORGANISM: Rattus Norvegicus
US-09-954-427A-238358

Alignment Scores:
Pred. No.: 716 Length: 25
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.20% Indels: 0
DB: 37 Gaps: 0

US-10-048-046-2 (1-664) x US-09-954-427A-238358 (1-25)

QY 300 GluthileuthrCvallelrcys 307
Db 2 GAGCACTAACCTGTATCATCTGT 25

RESULT 5
US-09-954-427A-238359
Sequence 238359, Application US/09954427A
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
TITLE OF INVENTION: Methods of Genetic Analysis of the Rat Genome
PAIR REFERENCE: 3112.1
CURRENT APPLICATION NUMBER: US/09/954,427A
CURRENT FILING DATE: 2001-09-17
PRIORITY NUMBER: 60/233,166
PRIORITY FILING DATE: 2000-09-18
NUMBER OF SEQ ID NOS: 420907
SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
SEQ ID NO 238359

Alignment Scores:
Pred. No.: 716 Length: 25
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.20% Indels: 0
DB: 37 Gaps: 0

US-09-954-427A-238359

ORGANISM: Rettub Norvegicus

Alignment Scores:
Pred. No.: 716 Length: 25
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.20% Indels: 0
DB: 37 Gaps: 0

US-09-954-427A-238359 (1-25)

QY 294 LypRPrbAlpLylMetGluIuLthr 301
Db 2 AACACGAGCAGATGGAGGAACA 25

RESULT 6
US-09-956-604-29770/C
Sequence 29770, Application US/09956604B
GENERAL INFORMATION:
APPLICANT: Mittmann, Michael
TITLE OF INVENTION: Methods of Genetic Analysis of the Rat Genome
PAIR REFERENCE: 3112.1
CURRENT APPLICATION NUMBER: US/09/956,604
CURRENT FILING DATE: 2001-09-19
PRIORITY NUMBER: 60/234,049
PRIORITY FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 141629
SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
PAIR REFERENCE: 3117.1
CURRENT APPLICATION NUMBER: US/09/956,604
CURRENT FILING DATE: 2001-09-19
PRIORITY NUMBER: 60/234,049
PRIORITY FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 141629
SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1

Alignment Scores:
; SEQ ID NO 29770
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-956-604-29770

Alignment Scores:
Pred. No.: 716 Length: 25
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.20% Indels: 0
DB: 38 Gaps: 0

US-10-048-046-2 (1-664) x US-09-956-604-29770 (1-25)

QY 462 SerThrSerValSerLeuThrThr 469
Db 25 AGTACGCCGATTCGCCTACTACA 2

RESULT 7
US-09-956-604A-29770/C
Sequence 29770, Application US/09956604A
GENERAL INFORMATION:
APPLICANT: Mittmann, Michael
TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
PAIR REFERENCE: 3117.1
CURRENT APPLICATION NUMBER: US/09/956,604A
CURRENT FILING DATE: 2001-09-19
PRIORITY NUMBER: 60/234,049
PRIORITY FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 141629
SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
SEQ ID NO 29770
LENGTH: 25
TYPE: DNA
ORGANISM: Escherichia coli
US-09-956-604A-29770

Alignment Scores:
Pred. No.: 716 Length: 25
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.20% Indels: 0
DB: 38 Gaps: 0

US-10-048-046-2 (1-664) x US-09-956-604A-29770 (1-25)

QY 462 SerThrSerValSerLeuThrThr 469
Db 25 AGTACGCCGATTCGCCTACTACA 2

RESULT 8
US-09-956-604B-29770/C
Sequence 29770, Application US/09956604B
GENERAL INFORMATION:
APPLICANT: Mittmann, Michael
TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
PAIR REFERENCE: 3117.1
CURRENT APPLICATION NUMBER: US/09/956,604B
CURRENT FILING DATE: 2001-09-19
PRIORITY NUMBER: 60/234,049
PRIORITY FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 141629
SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
SEQ ID NO 29770
LENGTH: 25
TYPE: DNA
ORGANISM: Escherichia coli
US-09-956-604B-29770

Alignment Scores:

```

Pred. No.: 716 Length: 25
 Score: 0.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.20^t Indels: 0
 DB: 38 Gaps: 0

RESULT 9 US-10-048-046-2 (1-664) x US-09-956-604B-29770 (1-25)
 US-10-719-956-88030
 Sequence 88030, Application US/10719956
 GENERAL INFORMATION:
 APPLICANT: Xue Mei Zhou
 TITLE OF INVENTION: Methods of Genetic Analysis of Rat
 FILE REFERENCE: 3527.1
 CURRENT APPLICATION NUMBER: US/10/719,956
 CURRENT FILING DATE: 2003-11-20
 PRIOR APPLICATION NUMBER: 60/427,836
 PRIOR FILING DATE: 2002-11-20
 NUMBER OF SEQ ID NOS: 699455
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 SEQ ID NO: 88030
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Rattus norvegicus
 US-10-719-956-88030
 Alignment Scores:
 Pred. No.: 716 Length: 25
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.20^t Indels: 0
 DB: 61 Gaps: 0

RESULT 10 US-10-048-046-2 (1-664) x US-10-719-956-88030 (1-25)
 Sequence 24277, Application US/11036317
 GENERAL INFORMATION:
 APPLICANT: Williams, Alan
 APPLICANT: Blume, John
 TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
 FILE REFERENCE: 3654.1
 CURRENT APPLICATION NUMBER: US/11/036,317
 CURRENT FILING DATE: 2005-01-13
 PRIOR APPLICATION NUMBER: US 60/536,639
 NUMBER OF SEQ ID NOS: 99174
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 SEQ ID NO: 24277
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Mus musculus
 US-11-036-317-24277
 Alignment Scores:
 Pred. No.: 716 Length: 25
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.20^t Indels: 0
 DB: 66 Gaps: 0

RESULT 11 US-10-048-046-2 (1-664) x US-11-036-317-24277 (1-25)
 US-11-036-317-24394
 Sequence 24394, Application US/11036317
 GENERAL INFORMATION:
 APPLICANT: Williams, Alan
 APPLICANT: Blume, John
 TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
 FILE REFERENCE: 3654.1
 CURRENT APPLICATION NUMBER: US/11/036,317
 CURRENT FILING DATE: 2005-01-13
 PRIOR APPLICATION NUMBER: US 60/536,639
 PRIOR FILING DATE: 2004-01-13
 NUMBER OF SEQ ID NOS: 99174
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 SEQ ID NO: 24394
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Mus musculus
 US-11-036-317-24394
 Alignment Scores:
 Pred. No.: 716 Length: 25
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.20^t Indels: 0
 DB: 66 Gaps: 0

RESULT 12 US-10-048-046-2 (1-664) x US-11-036-317-24394 (1-25)
 Sequence 60227, Application US/11036317
 GENERAL INFORMATION:
 APPLICANT: Williams, Alan
 APPLICANT: Blume, John
 TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
 FILE REFERENCE: 3654.1
 CURRENT APPLICATION NUMBER: US/11/036,317
 CURRENT FILING DATE: 2005-01-13
 PRIOR APPLICATION NUMBER: US 60/536,639
 NUMBER OF SEQ ID NOS: 99174
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 SEQ ID NO: 60227
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Mus musculus
 US-11-036-317-60227
 Alignment Scores:
 Pred. No.: 716 Length: 25
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.20^t Indels: 0
 DB: 66 Gaps: 0

RESULT 13 US-10-048-046-2 (1-664) x US-11-036-317-60227 (1-25)
 Sequence 49, Application US/11036317
 GENERAL INFORMATION:
 APPLICANT: Williams, Alan
 APPLICANT: Blume, John
 TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
 FILE REFERENCE: 3654.1
 CURRENT APPLICATION NUMBER: US/11/036,317
 CURRENT FILING DATE: 2005-01-13
 PRIOR APPLICATION NUMBER: US 60/536,639
 NUMBER OF SEQ ID NOS: 99174
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 SEQ ID NO: 49
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Mus musculus
 US-11-036-317-49
 Alignment Scores:
 Pred. No.: 716 Length: 25
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.20^t Indels: 0
 DB: 66 Gaps: 0

Db 1 TCTTTCGGCAGCAATAACTGGTC 24
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIORITY APPLICATION NUMBER: US 60/536,639
; PRIORITY FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
; SEQ ID NO 61246
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-11-036-317-61246
Alignment Scores:
Pred. No.: 716 Length: 25
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.20% Indels: 0
DB: 66 Gaps: 0
US-10-048-046-2 (1-664) x US-11-036-317-61246 (1-25)
Qy 47 AspLeuSerPheProSerAsnIys 54
Db 2 GACCTCTTCCAGCATAA 25
RESULT 14
US-11-036-317-67592
Sequence 67592, Application US/11036317
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OR INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIORITY APPLICATION NUMBER: US 60/536,639
PRIORITY FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
SEQ ID NO 67592
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-67592
Sequence 67592, Application US/11036317
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OR INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIORITY APPLICATION NUMBER: US 60/536,639
PRIORITY FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
SEQ ID NO 67592
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-67592
Alignment Scores:
Pred. No.: 716 Length: 25
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.20% Indels: 0
DB: 66 Gaps: 0
US-10-048-046-2 (1-664) x US-11-036-317-108822 (1-25)
Qy 388 AspMetLeuGlnProArgValAlaArg 395
Db 1 GATATGTGCAACCAAGTCAGG 24
Search completed: January 12, 2006, 13:29:43
Job time : 8982 secB

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 12, 2006, 10:27:18 ; Search time 130 Seconds

(without alignments)
2639.356 Million cell updates/sec

Title: US-10-048-046-2

Perfect score: 664

Sequence: 1 MESPREGKQSPPPQWPGRLL..... VKAHHAHAKPNHICOTPKN 664

Score: 664

Xgapext 60.0 Xgapext 60.0

Ygapop 60.0 Ygapext 60.0

Rgapop 6.0 Rgapext 7.0

Delop 6.0 Delext 7.0

Searched: 1087749 seqs, 258370665 residues

Post-processing: Listing first 45 summaries

Command line parameters:

Total number of hits satisfying chosen parameters: 208730

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Pending Patents NA New:*

1 /cgm2_6/pctdata/1/pna/PCT NEW COMB. SEQ:*

2 /cgm2_6/pctdata/1/pna/US36 NEW COMB. SEQ:*

3 /cgm2_6/pctdata/1/pna/US37 NEW COMB. SEQ:*

4 /cgm2_6/pctdata/1/pna/US38 NEW COMB. SEQ:*

5 /cgm2_6/pctdata/1/pna/US39 NEW COMB. SEQ:*

6 /cgm2_6/pctdata/1/pna/US30 NEW COMB. SEQ:*

7 /cgm2_6/pctdata/1/pna/US31 NEW COMB. SEQ:*

8 /cgm2_6/pctdata/1/pna/US32 NEW COMB. SEQ:*

-PGREXTX-7 -YGRPOP-60 -YKAREXTX-60 -DRGOp6 -DLExt7

Database : Pending Patents NA New:*

1 /cgm2_6/pctdata/1/pna/PCT NEW COMB. SEQ:*

2 /cgm2_6/pctdata/1/pna/US36 NEW COMB. SEQ:*

3 /cgm2_6/pctdata/1/pna/US37 NEW COMB. SEQ:*

4 /cgm2_6/pctdata/1/pna/US38 NEW COMB. SEQ:*

5 /cgm2_6/pctdata/1/pna/US39 NEW COMB. SEQ:*

6 /cgm2_6/pctdata/1/pna/US30 NEW COMB. SEQ:*

7 /cgm2_6/pctdata/1/pna/US31 NEW COMB. SEQ:*

8 /cgm2_6/pctdata/1/pna/US32 NEW COMB. SEQ:*

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | Length | DB ID | Description |
|------------|-------|-------|--------|-------|--|
| C 1 | 6 | 0.9 | 19 | 6 | US-10-562-561-562 Sequence 562, APP |
| C 2 | 6 | 0.9 | 19 | 6 | US-10-562-561-887 Sequence 887, APP |
| C 3 | 6 | 0.9 | 20 | 6 | US-10-527-552-18 Sequence 18, APP |
| C 4 | 6 | 0.9 | 20 | 7 | US-11-294-621-70 Sequence 70, APP |
| C 5 | 6 | 0.9 | 20 | 7 | US-11-317-798-553 Sequence 553, APP |
| C 6 | 6 | 0.9 | 21 | 8 | US-60-742-219-4800 Sequence 4800, APP |
| C 7 | 6 | 0.9 | 22 | 7 | US-11-130-645B-10537 Sequence 8449, APP |
| C 8 | 6 | 0.9 | 22 | 7 | US-11-130-645B-10537 Sequence 10537, APP |
| C 9 | 6 | 0.9 | 22 | 7 | US-11-130-645B-10712 Sequence 10712, APP |
| C 10 | 6 | 0.9 | 22 | 7 | US-11-130-645B-13922 Sequence 13922, APP |

RESULT 1
US-10-562-561-562/C
; Sequence 562, Application US/10562561
; GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Treatment of Alzheimer's Disease Using
FILE REFERENCE: 400/166 (MBIB02-728-Q)
CURRENT APPLICATION NUMBER: US/10/562, 561
CURRENT FILING DATE: 2005-12-28
PRIOR APPLICATION NUMBER: US 10/607933
PRIOR FILING DATE: 2003-06-27
PRIOR APPLICATION NUMBER: US 09/930423
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: PCT/US03/04710
PRIOR APPLICATION NUMBER: US 10/205309
PRIOR FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: PCT/US04/16390
PRIOR FILING DATE: 2004-05-24
PRIOR APPLICATION NUMBER: US 10/826966
PRIOR FILING DATE: 2004-04-15
PRIOR APPLICATION NUMBER: US 10/757803
PRIOR FILING DATE: 2004-01-14
PRIOR APPLICATION NUMBER: US 10/720448
PRIOR FILING DATE: 2003-11-24
PRIOR APPLICATION NUMBER: US 10/693059
PRIOR FILING DATE: 2003-10-23
PRIOR APPLICATION NUMBER: US 10/44853
PRIOR FILING DATE: 2003-01-23
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1904

ALIGNMENTS

| | | | | | |
|----|---|-----|----|---|--|
| 11 | 6 | 0.9 | 22 | 7 | US-11-110-645B-13924 Sequence 13924, A |
| 12 | 6 | 0.9 | 22 | 7 | US-11-130-645B-13926 Sequence 13926, A |
| 13 | 6 | 0.9 | 22 | 7 | US-11-130-645B-16045 Sequence 16045, A |
| 14 | 6 | 0.9 | 23 | 6 | US-10-515-051-78 Sequence 78, APP |
| 15 | 6 | 0.9 | 25 | 7 | US-11-067-260-59 Sequence 59, APP |
| 16 | 6 | 0.9 | 25 | 7 | US-11-067-260-61 Sequence 61, APP |
| 17 | 6 | 0.9 | 25 | 7 | US-11-067-260-65 Sequence 65, APP |
| 18 | 6 | 0.9 | 25 | 7 | US-11-067-260-67 Sequence 67, APP |
| 19 | 6 | 0.9 | 25 | 7 | US-11-067-260-92 Sequence 92, APP |
| 20 | 6 | 0.9 | 25 | 7 | US-11-315-777-1 Sequence 1, APP |
| 21 | 6 | 0.9 | 25 | 7 | US-11-319-873-1 Sequence 12, APP |
| 22 | 6 | 0.9 | 25 | 8 | US-60-735-552-12 Sequence 37, APP |
| 23 | 6 | 0.9 | 26 | 7 | US-10-149-533B-37 Sequence 1077, APP |
| 24 | 6 | 0.9 | 27 | 7 | US-11-317-798-5547 Sequence 5547, APP |
| 25 | 6 | 0.9 | 29 | 7 | PCT-US05-10312-241 Sequence 2441, APP |
| 26 | 6 | 0.9 | 30 | 8 | US-60-751-196-10 Sequence 10, APP |
| 27 | 6 | 0.9 | 30 | 8 | US-60-751-196-15 Sequence 15, APP |
| 28 | 6 | 0.9 | 30 | 8 | US-11-275-240-75 Sequence 109, APP |
| 29 | 6 | 0.9 | 31 | 7 | US-11-262-204-10 Sequence 2, APP |
| 30 | 6 | 0.9 | 33 | 7 | US-11-067-260-46-2 Sequence 75, APP |
| 31 | 6 | 0.9 | 34 | 7 | US-11-317-798-3675 Sequence 3675, APP |
| 32 | 6 | 0.9 | 34 | 7 | US-11-067-260-12 Sequence 12, APP |
| 33 | 6 | 0.9 | 35 | 5 | US-09-142-471D-12 Sequence 13, APP |
| 34 | 6 | 0.9 | 35 | 7 | US-11-067-260-111 Sequence 11, APP |
| 35 | 6 | 0.9 | 35 | 7 | US-11-317-798-5302 Sequence 5302, APP |
| 36 | 6 | 0.9 | 38 | 7 | US-11-067-260-106 Sequence 106, APP |
| 37 | 6 | 0.9 | 38 | 7 | US-11-067-260-73 Sequence 73, APP |
| 38 | 6 | 0.9 | 39 | 7 | US-11-067-260-63 Sequence 63, APP |
| 39 | 6 | 0.9 | 41 | 7 | US-11-067-260-69 Sequence 69, APP |
| 40 | 6 | 0.9 | 41 | 7 | US-11-067-260-77 Sequence 77, APP |
| 41 | 6 | 0.9 | 41 | 7 | US-11-067-260-87 Sequence 87, APP |
| 42 | 6 | 0.9 | 42 | 6 | US-10-199-920A-102 Sequence 102, APP |
| 43 | 6 | 0.9 | 42 | 7 | US-11-067-260-94 Sequence 94, APP |
| 44 | 6 | 0.9 | 42 | 7 | US-11-067-260-94 Sequence 94, APP |
| 45 | 6 | 0.9 | 42 | 7 | US-11-067-260-94 Sequence 94, APP |

SOFTWARE: PatentIn version 3.3
 SEQ ID NO 562
 LENGTH: 19
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/sINA sense r
 US-10-562-561-562

Alignment Scores:
 Pred. No.: 885 Length: 19
 Score: 6.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.90% Indels: 0
 DB: 6 Gaps: 0

US-10-048-046-2 (1-664) x US-10-562-561-562 (1-19)

Qy 193 ThrlGlutProserProala 198
 Db 19 ACAGAGCCAGCCCTGT 2

RESULT 2
 US-10-562-561-887
 Sequence 887, Application US/10562561
 GENERAL INFORMATION:
 APPLICANT: SINA Therapeutics, Inc.
 APPLICANT: McSwiggan, James
 APPLICANT: Beigelman, Leonid
 TITLE OF INVENTION: RNA Interference Mediated Treatment of Alzheimer's Disease Using Short Interfering Nucleic Acid (sINA)
 TITLE OF INVENTION: Short Interfering Nucleic Acid (sINA)
 PFL REFERENCE: 400/166 (MABR02178-G)
 CURRENT APPLICATION NUMBER: US/10/562,561
 CURRENT FILING DATE: 2005-12-28
 PRIOR APPLICATION NUMBER: US 10/607933
 PRIOR FILING DATE: 2003-06-27
 PRIOR APPLICATION NUMBER: US 09/930423
 PRIOR FILING DATE: 2001-08-15
 PRIOR APPLICATION NUMBER: PCT/US63/04710
 PRIOR FILING DATE: 2003-02-18
 PRIOR APPLICATION NUMBER: US 10/205309
 PRIOR FILING DATE: 2002-07-25
 PRIOR APPLICATION NUMBER: PCT/US04/16390
 PRIOR FILING DATE: 2004-05-24
 PRIOR APPLICATION NUMBER: US 10/226966
 PRIOR FILING DATE: 2004-04-16
 PRIOR APPLICATION NUMBER: US 10/757803
 PRIOR FILING DATE: 2004-01-14
 PRIOR APPLICATION NUMBER: US 10/20448
 PRIOR FILING DATE: 2003-11-24
 PRIOR APPLICATION NUMBER: US 10/693059
 PRIOR FILING DATE: 2003-10-23
 PRIOR APPLICATION NUMBER: US 10/444853
 PRIOR FILING DATE: 2003-05-23
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 1904
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO 887
 LENGTH: 19
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: sINA antisense region
 US-10-562-561-887

Alignment Scores:
 Pred. No.: 885 Length: 19
 Score: 6.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.90% Indels: 0
 DB: 6 Gaps: 0

US-10-048-046-2 (1-664) x US-10-527-552-18 (1-19)

Qy 208 Serglyglyglyglylyle 213
 Db 1 TCGGGAGGTGGGAAATT 18

RESULT 3
 US-10-527-552-18
 Sequence 18, Application US/10527552
 GENERAL INFORMATION:
 APPLICANT: Sandoz GmbH
 TITLE OF INVENTION: Process for production of cephalosporin C
 FILE REFERENCE: IB/G-32677A/BCK
 CURRENT APPLICATION NUMBER: US/10/527,552
 CURRENT FILING DATE: 2005-03-11
 NUMBER OF SEQ ID NOS: 21
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 18
 LENGTH: 20
 TYPE: DNA
 ORGANISM: Artificial
 FEATURE:
 OTHER INFORMATION: oligonucleotide primer
 US-10-527-552-18

Alignment Scores:
 Pred. No.: 926 Length: 20
 Score: 6.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.90% Indels: 0
 DB: 6 Gaps: 0

US-10-048-046-2 (1-664) x US-10-527-552-18 (1-20)

Qy 208 Serglyglyglyglylyle 213
 Db 1 TCGGGAGGTGGGAAATT 18

RESULT 4
 US-11-294-621-70/c
 Sequence 70, Application US/11294621
 GENERAL INFORMATION:
 APPLICANT: BELL, DAPHNE WINIFRED
 APPLICANT: HABER, DANIEL A.
 APPLICANT: JANE, PAST ANTERO
 APPLICANT: JOHNSON, BRUCE E.
 APPLICANT: LYNCH, THOMAS J.
 APPLICANT: MEYERSON, MATTHEW
 APPLICANT: PARZ, JUAN GUILLERMO
 APPLICANT: SELLERS, WILLIAM R.
 APPLICANT: SETTELMAN, JEFFREY B.
 APPLICANT: SORDELLA, RAFFAELLA
 TITLE OF INVENTION: METHOD TO DETERMINE RESPONSIVENESS OF CANCER TO EPIDERMAL GROWTH FACTOR RECEPTOR TARGETING TREATMENTS
 TITLE OF INVENTION: TREATMENTS
 FILE REFERENCE: 030258-055147
 CURRENT APPLICATION NUMBER: US/11/294,621
 CURRENT FILING DATE: 2005-12-05
 PRIOR APPLICATION NUMBER: PCT/US05/016645
 PRIOR FILING DATE: 2005-03-31
 PRIOR APPLICATION NUMBER: 60/558,218
 PRIOR FILING DATE: 2004-03-31
 PRIOR APPLICATION NUMBER: 60/561,095
 PRIOR FILING DATE: 2004-04-09
 PRIOR APPLICATION NUMBER: 60/565,753
 PRIOR FILING DATE: 2004-04-27
 PRIOR APPLICATION NUMBER: 60/565,985
 PRIOR FILING DATE: 2004-04-27
 PRIOR APPLICATION NUMBER: 60/574,035
 PRIOR FILING DATE: 2004-05-25
 PRIOR APPLICATION NUMBER: 60/577,916

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    / PRIOR FILING DATE: 2004-06-07
    / PRIOR APPLICATION NUMBER: 60/592,287
    / PRIOR FILING DATE: 2004-07-29
    / NUMBER OF SEQ ID NOS: 762
    / SOFTWARE: Patentin Ver. 3.3
    / SEQ ID NO: 70
    / LENGTH: 20
    / TYPE: DNA
    / ORGANISM: Homo sapiens
    / US-11-294-621-70

Alignment Scores:
Pred. No.:          926      Length:      20
Score:             6.00     Matches:      6
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:       0.90%  Indels:      0
DB:                7        Gaps:       0
US-10-048-046-2 (1-664) x US-11-294-621-70 (1-20)

Qy    77 ThrSerThrBerglyThr 82
Db   19 ACTTCGACTCTGGGCACTA 2

RESULT 5
US-11-317-798-5513
/ Sequence 5513, Application US/11317798
/ GENERAL INFORMATION:
/ APPLICANT: Lofton-Day, Cathy; Model, Fabian; Sledziewski, Juergen
/ APPLICANT: Andrew, Rulan; Tamer, Levin; Joern, Dieter; Juergen
/ APPLICANT: Andrew, Rulan; Tamer, Levin; Joern, Dieter; Juergen
/ TITLE OF INVENTION: Methods and nucleic acids for the analysis of colon cell
/ FILE REFERENCE: 47675-174
/ CURRENT APPLICATION NUMBER: US/11/317,798
/ CURRENT FILING DATE: 2005-12-23
/ PRIOR APPLICATION NUMBER: US 10/603,138
/ PRIOR FILING DATE: 2003-06-23
/ PRIOR APPLICATION NUMBER: PCT/US04/20336
/ PRIOR FILING DATE: 2004-06-23
/ PRIOR APPLICATION NUMBER: US 10/602,494
/ PRIOR APPLICATION NUMBER: EP 04090175,3
/ PRIOR FILING DATE: 2004-05-06
/ PRIOR APPLICATION NUMBER: EP 04090072,2
/ PRIOR FILING DATE: 2004-02-27
/ NUMBER OF SEQ ID NOS: 14624
/ SEQ ID NO 5513
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial sequence
/ FEATURE: biotinylated treated
/ OTHER INFORMATION: nucleic acid for analysis of methylation status of SEQ ID NO: 45
/ OTHER INFORMATION: nucleic acid for analysis of methylation status of SEQ ID NO: 45

Alignment Scores:
Pred. No.:          926      Length:      20
Score:             6.00     Matches:      6
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:       0.90%  Indels:      0
DB:                7        Gaps:       0
US-11-317-798-5513

RESULT 6
US-60-742-219-4800
/ Sequence 60-742-219-4800
/ GENERAL INFORMATION:
/ APPLICANT: Belouchi, Abdelmajid
/ APPLICANT: Raelson, John Verner
/ APPLICANT: Bradley, Walter Edward
/ APPLICANT: Paquin, Bruno
/ APPLICANT: Nguyen-Huu, Quynh
/ APPLICANT: Croteau, Pascal
/ APPLICANT: Allard, Rene
/ APPLICANT: Little, Randall David
/ APPLICANT: Keith, Tim
/ APPLICANT: Cousineau, Johanne
/ APPLICANT: Berdewegh, Paul Van
/ APPLICANT: Segal, Jonathan
/ TITLE OF INVENTION: Gene Map of the Human Genes Associated with Psoriasis
/ FILE REFERENCE: 306522-2000
/ CURRENT APPLICATION NUMBER: US/60/742,219
/ CURRENT FILING DATE: 2005-12-05
/ NUMBER OF SEQ.ID NOS: 7303
/ SOFTWARE: Patentin version 3.3
/ SEQ ID NO 6000
/ LENGTH: 21
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-60-742-219-4800

RESULT 7
US-11-130-645B-8449
/ Sequence 8449, Application US/11130645B
/ GENERAL INFORMATION:
/ APPLICANT: ROSETTA GENOMICS LTD
/ TITLE OF INVENTION: MICRORNAs AND USES THEREOF
/ FILE REFERENCE: 06087.0202.CPUS13
/ CURRENT APPLICATION NUMBER: US/11/130,645B
/ CURRENT FILING DATE: 2005-05-16
/ NUMBER OF SEQ ID NOS: 760513
/ SOFTWARE: Patentin version 3.3
/ SEQ ID NO 8449
/ LENGTH: 22
/ TYPE: RNA
/ ORGANISM: Homo sapiens
/ US-11-130-645B-8449

Alignment Scores:
Pred. No.:          926      Length:      22
Score:             6.00     Matches:      6
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:       0.90%  Indels:      0
DB:                7        Gaps:       0
US-10-048-046-2 (1-664) x US-11-130-645B-8449 (1-20)

Qy    394 ValAlaGArgRArgPhaser 399
Db   1 GTGAGACGTCTTCCTTG 18

RESULT 8
US-11-130-645B-10537
/ Sequence 10537, Application US/11130645B
/ GENERAL INFORMATION:
/ APPLICANT: Belouchi, Abdelmajid
/ APPLICANT: Raelson, John Verner
/ APPLICANT: Bradley, Walter Edward
/ APPLICANT: Paquin, Bruno
/ APPLICANT: Nguyen-Huu, Quynh
/ APPLICANT: Croteau, Pascal
/ APPLICANT: Allard, Rene
/ APPLICANT: Little, Randall David
/ APPLICANT: Keith, Tim
/ APPLICANT: Cousineau, Johanne
/ APPLICANT: Berdewegh, Paul Van
/ APPLICANT: Segal, Jonathan
/ TITLE OF INVENTION: Gene Map of the Human Genes Associated with Psoriasis
/ FILE REFERENCE: 306522-2000
/ CURRENT APPLICATION NUMBER: US/60/742,219
/ CURRENT FILING DATE: 2005-12-05
/ NUMBER OF SEQ.ID NOS: 7303
/ SOFTWARE: Patentin version 3.3
/ SEQ ID NO 6000
/ LENGTH: 21
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-60-742-219-4800

Alignment Scores:
Pred. No.:          926      Length:      21
Score:             6.00     Matches:      6
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:       0.90%  Indels:      0
DB:                7        Gaps:       0
US-10-048-046-2 (1-664) x US-11-130-645B-8449 (1-22)

Qy    3 ArgProGluGluGlyLys 8
Db   4 AGGCCAGAGGGGAGG 21

```

US-11-130-645B-13922
 APPLICANT: ROSETTA GENOMICS LTD
 TITLE OF INVENTION: MICRORNAs AND USES THEREOF
 FILE REFERENCE: 06087_0202_CPUS13
 CURRENT APPLICATION NUMBER: US/11/130,645B
 CURRENT FILING DATE: 2005-05-16
 NUMBER OF SEQ ID NOS: 760616
 SEQ ID NO 10337
 LENGTH: 22
 TYPE: RNA
 ORGANISM: Homo sapiens
 US-11-130-645B-10537
 Alignment Scores:
 Pred. No.: 1.01e+03 Length: 22
 Score: 6.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.90% Indels: 0
 DB: Gaps: 0
 US-10-048-046-2 (1-664) x US-11-130-645B-10537 (1-22)
 Qy 195 ProSeProAlaGlyArg 200
 Db 5 CCCUCUCUGUGGGCA 22
 RESULT 9
 US-11-130-645B-10712/c
 Sequence 13922 Application US/11130645B
 GENERAL INFORMATION:
 APPLICANT: ROSETTA GENOMICS LTD
 TITLE OF INVENTION: MICRORNAs AND USES THEREOF
 FILE REFERENCE: 06087_0202_CPUS13
 CURRENT APPLICATION NUMBER: US/11/130,645B
 CURRENT FILING DATE: 2005-05-16
 NUMBER OF SEQ ID NOS: 760616
 SEQ ID NO 10712
 LENGTH: 22
 TYPE: RNA
 ORGANISM: Homo sapiens
 US-11-130-645B-10712
 Alignment Scores:
 Pred. No.: 1.01e+03 Length: 22
 Score: 6.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.90% Indels: 0
 DB: Gaps: 0
 US-10-048-046-2 (1-664) x US-11-130-645B-10712 (1-22)
 Qy 452 GlyAlaProGalaLeu 457
 Db 22 dgcgtcccccacccctc 5
 RESULT 10
 US-11-130-645B-13922
 Sequence 13922 Application US/11130645B
 GENERAL INFORMATION:
 APPLICANT: ROSETTA GENOMICS LTD
 TITLE OF INVENTION: MICRORNAs AND USES THEREOF
 FILE REFERENCE: 06087_0202_CPUS13
 CURRENT APPLICATION NUMBER: US/11/130,645B
 CURRENT FILING DATE: 2005-05-16
 NUMBER OF SEQ ID NOS: 760616
 SEQ ID NO 13922
 LENGTH: 22
 TYPE: RNA
 ORGANISM: Homo sapiens
 US-11-130-645B-13924
 Sequence 13924 Application US/11130645B
 GENERAL INFORMATION:
 APPLICANT: ROSETTA GENOMICS LTD
 TITLE OF INVENTION: MICRORNAs AND USES THEREOF
 FILE REFERENCE: 06087_0202_CPUS13
 CURRENT APPLICATION NUMBER: US/11/130,645B
 CURRENT FILING DATE: 2005-05-16
 NUMBER OF SEQ ID NOS: 760616
 SEQ ID NO 13924
 LENGTH: 22
 TYPE: RNA
 ORGANISM: Homo sapiens
 US-11-130-645B-13924
 Alignment Scores:
 Pred. No.: 1.01e+03 Length: 22
 Score: 6.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.90% Indels: 0
 DB: Gaps: 0
 US-10-048-046-2 (1-664) x US-11-130-645B-13924 (1-22)
 Qy 368 AspLeuSerArgSerGlu 373
 Db 5 GAAAGCUACAGGUCUCA 22
 RESULT 12
 US-11-130-645B-13926
 Sequence 13926 Application US/11130645B
 GENERAL INFORMATION:
 APPLICANT: ROSETTA GENOMICS LTD
 TITLE OF INVENTION: MICRORNAs AND USES THEREOF
 FILE REFERENCE: 06087_0202_CPUS13
 CURRENT APPLICATION NUMBER: US/11/130,645B
 CURRENT FILING DATE: 2005-05-16
 NUMBER OF SEQ ID NOS: 760616
 SEQ ID NO 13926
 LENGTH: 22
 TYPE: RNA
 ORGANISM: Homo sapiens
 US-11-130-645B-13926
 Alignment Scores:
 Pred. No.: 1.01e+03 Length: 22
 Score: 6.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 0.90% Indels: 0
 DB: Gaps: 0
 US-10-048-046-2 (1-664) x US-11-130-645B-13926 (1-22)

OY 368 Abolysserarginberglu 373
Db 5 GAAUAGCUAGGUCUGAU 22

RESULT 13
Sequence 16045, Application US/11130645B
GENERAL INFORMATION:
APPLICANT: ROBETTA GENOMICS LTD
TITLE OF INVENTION: MICRORNAs AND USBS THEREOF
FILE REFERENCE: 06087-0202.CPUS13
CURRENT APPLICATION NUMBER: US/11/130,645B
CURRENT FILING DATE: 2005-05-16
NUMBER OF SEQ ID NOS: 760616 ;
SEQ ID NO 16045
LENGTH: 22
TYPE: RNA
ORGANISM: Homo sapiens
US-11-130-645B-16045

Alignment Scores:
Pred. No.: 1.01e+03 Length: 22
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.90% Indels: 0
DB: 7 Gaps: 0

RESULT 14
US-10-515-051-78
Sequence 78, Application US/10515051
GENERAL INFORMATION:
APPLICANT: OINO, Ryozo
APPLICANT: TSURUO, Takashi
APPLICANT: NAKAMURA, Yusuke
TITLE OF INVENTION: METHOD FOR JUDGING SENSIBILITY TO IMATINIB
FILE REFERENCE: 0760-0142.PUS1
CURRENT APPLICATION NUMBER: US/10/515,051
CURRENT FILING DATE: 2004-11-19
PRIOR APPLICATION NUMBER: PCT/JP03/06330
PRIOR FILING DATE: 2003-05-21
SEQ ID NO 78
NUMBER OF SEQ ID NOS: 154
LENGTH: 23
TYPE: DNA
FEATURE:
ORGANISM: Artificial sequence
OTHER INFORMATION: A oligonucleotide reverse primer used for amplifying human CTSG cDNA
US-10-515-051-78

Alignment Scores:
Pred. No.: 1.05e+03 Length: 23
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.90% Indels: 0
DB: 6 Gaps: 0

RESULT 15
US-11-067-260-59
Sequence 59, Application US/11067260
GENERAL INFORMATION:
APPLICANT: AXICO, Maria
TITLE OF INVENTION: HETEROLOGOUS EXPRESSION OF NEISSERIAL PROTEINS
FILE REFERENCE: 223002099501
CURRENT APPLICATION NUMBER: US/11/067, 260
CURRENT FILING DATE: 2005-02-25
PRIORITY NUMBER: 10/220,480
PRIORITY FILING DATE: 2002-08-28
PRIORITY APPLICATION NUMBER: PCT/IB01/00420
PRIORITY FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.2
SEQ ID NO 59
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: fu (961)-741(MCS58)-H18 Fwd
US-11-067-260-59

Alignment scores:
Pred. No.: 1.13e+03 Length: 25
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.90% Indels: 0
DB: 7 Gaps: 0

RESULT 16
US-10-048-046-2 (1-664) x US-11-130-645B-16045 (1-22)
OY 161 ValProProSerGlu 166
Db 5 GUCCUCUCCGUCA 22

RESULT 17
US-10-048-046-2 (1-664) x US-11-067-260-59 (1-25)
OY 207 GlySerGlyGlyGlyGly 212
Db 4 GGATCCGGAGGGGT 21

Search completed: January 12, 2006, 13:31:58
Job time : 130 secs